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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/212,270

DATE: 04/08/1999

TIME: 09:16:10

Input Set: I212270.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

ENTERED

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1  <110> APPLICANT: Catherine Tribouley
2      David Pot
3      Altaf Kassam
4      George Lamson
5  <120> TITLE OF INVENTION: New Members of TNF and TNFR Families
6  <130> FILE REFERENCE: 1408-002
7  <140> CURRENT APPLICATION NUMBER: US/09/212,270
8  <141> CURRENT FILING DATE: 1998-12-16
9  <160> NUMBER OF SEQ ID NOS: 16
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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12 <211> LENGTH: 285
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19              20              25              30
20      Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
21              35              40              45
22      Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
23              50              55              60
24      Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
25      65              70              75              80
26      Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
27              85              90              95
28      Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
29              100             105             110
30      Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
31              115             120             125
32      Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
33              130             135             140
34      Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
35      145             150             155             160
36      Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
37              165             170             175
38      Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
39              180             185             190
40      Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
41              195             200             205
42      Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
43              210             215             220
44      Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu

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45      225      230      235      240
46      Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
47              245      250      255
48      Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
49              260      265      270
50      Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
51              275      280      285
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53 <211> LENGTH: 153
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55 <213> ORGANISM: human
56 <400> SEQUENCE: 2
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60              20              25              30
61      Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys
62              35              40              45
63      Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr
64      50              55              60
65      Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser
66      65              70              75              80
67      Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala
68              85              90              95
69      Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys
70              100              105              110
71      Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu
72              115              120              125
73      Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg
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75      Leu Gln Arg Leu Leu Gln Ala Leu Glu
76      145              150
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80 <213> ORGANISM: human
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85              20              25              30
86      Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
87      35              40              45
88      Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
89      50              55              60
90      Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
91      65              70              75              80
92      Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
93              85              90              95
94      Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala

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95          100          105          110
96    Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
97          115          120          125
98    Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
99          130          135          140
100   Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser
101   145          150          155          160
102   Thr Val Ser Ser Pro Arg Asp Thr Ala Val Ala Ala Val Ile Cys Ser
103          165          170          175
104   Ala Leu Ala Thr Val Leu Leu Ala Cys Ser Ser Cys Val Ser Ser Thr
105          180          185          190
106   Ala Arg Gly Ser Ser Trp Arg Arg Asn Pro Ala Val Ser Ser His Pro
107          195          200          205
108   Ser Val
109          210
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111   <211> LENGTH: 151
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117   Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
118          20          25          30
119   Asp Cys Ser Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val
120          35          40          45
121   Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly
122          50          55          60
123   Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg
124          65          70          75          80
125   Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys
126          85          90          95
127   Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp
128          100          105          110
129   Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu
130          115          120          125
131   Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro
132          130          135          140
133   Pro Tyr Glu Pro His Cys Glu
134          145          150
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141       1          5          10          15
142   Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly
143          20          25          30
144   Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala

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145          35          40          45
146      Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln
147          50          55          60
148      Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala
149      65          70          75          80
150      Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala
151          85          90          95
152      Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile
153          100          105          110
154      Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp
155          115          120          125
156      Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg
157          130          135          140
158      Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp
159      145          150          155          160
160      Arg Ala Tyr Asn Ser Gln Tyr Ser Ala Gly Val Pro His Leu His Gln
161          165          170          175
162      Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn
163          180          185          190
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165          195          200          205
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173      taaatgccag caaacctact gtacagtagg ggtagagatg cagaaaaggca gaaaggagaa      180
174      aattcaggat aactctcctg aggggtgagc caagccctgc catgtagtgc acgcaggaca      240
175      tcaacaaaca cagataacag gaaatgatcc attccctgtg gtcacttatt ctaaaaggccc      300
176      caaccttcaa agttcaagta gtgatatgga tgactccaca gaaagggagc agtcacgcct      360
177      tactttcttg ctttaagaaa gagaagaaat gaaactgaag gagtgtgttt ccattcctccc      420
178      acggaaggaa agcccctctg tccgatcctc caaagacgga aagctgctgg ctgcaacctt      480
179      gctgctggca ctgctgtctt gctgcctcac ggtggtgtct ttctaccagg tggccgccct      540
180      gcaaggggac ctggccagcc tccgggcaga gctgcagggc caccacgcgg agaagctgcc      600
181      agcaggagca ggagcccccaggccgcct ggaggaagct ccagctgtca ccgcgggact      660
182      gaaaaatcttt gaaccaccag ctccaggaga aggcaactcc agtcagaaca gcagaaataa      720
183      gcgtgccgtt cagggtccag aagaaacagt cactcaagac tgcttgcaac tgattgcaga      780
184      cagtgaacaa ccaactatac aaaaaggatc ttacacattt gttccatggc ttctcagctt      840
185      taaaaggggga agtgccttag aagaaaaaga gaataaaata ttggtcaaag aaactgggta      900
186      cttttttata tatggtcagg ttttatatac tgataagacc tacgccatgg gacatctaata      960
187      tcagaggaag aaggtccatg tctttgggga tgaattgagt ctggtgactt tgtttcgatg      1020
188      tattcaaaat atgcctgaaa cactacccaa taattcctgc tattcagctg gcattgcaaa      1080
189      actggaagaa ggagatgaac tccaacttgc aataccaaga gaaaatgcac aaatatcact      1140
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191      tgtagctatt ttcctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac      1260
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194 <211> LENGTH: 459

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200      ttctgcttgg agcacgcacg gtgtccacct ggtgccggcg tgattgcccc gggcaccccc      180
201      agccagaaca cgcagtgccg gccgtgcccc ccaggcacct tctcagccag cagctccagc      240
202      tcagagcagt gccagcccca ccgcaactgc acggccctgg gcctggccct caatgtgccg      300
203      ggctcttcct cccatgacac cctgtgcacc agctgcactg gcttccccct cagcaccagg      360
204      gtaccaggag ctgaggagtg tgagcgtgcc gtcacgactt ttgtggcttt ccaggacatc      420
205      tccatcaaga ggctgcagcg gctgctgcag gccctcgag      459
206 <210> SEQ ID NO 8
207 <211> LENGTH: 893
208 <212> TYPE: DNA
209 <213> ORGANISM: human
210 <400> SEQUENCE: 8
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213      ctggcatgta aagtgagttg cgaaaccgga gattgcaggc agcaggaatt caaggatcga      180
214      tctggaaact gtgtcctctg caaacagtgc ggacctggca tggagttgtc caaggaatgt      240
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224      tacaagatgc aggaaaacga gcctcttcag gaatctcagg gcctcctagg gatgctggca      840
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233      actcaaggtc ctacctctac acaggacggt gctcttcgct gccattctct tcctactcca      180
234      cctggcatgt aaagtgagtt gcgaaaaccg agattgcagg cagcaggaat tcaaggatcg      240
235      atctggaaac tgtgtcctct gcaaacagtgc cggacctggc atggagttgt ccaaggaaatg      300
236      tggcttcggc tatggggagg atgcacagtg tgtgccctgc aggccgcacc ggttcaaggaa      360
237      agactggggt ttccagaagt gtaagccatg tcgggactgt gcgctggtga accgctttca      420
238      gagggccaac tgctcacaca ccagtgatgc tgtctgcggg gactgcctgc caggatttta      480
239      ccggaagacc aaactggttg gttttcaaga catggagtgt gtgccctgcg gagaccaccc      540
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243 <211> LENGTH: 1260
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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
